

1000

21356245.f MLDNFVTKPSTRS-SPPPGARKSDRVSSPLVLVDVTETAEHPLS-PMPEPSPPIIDLNLNQPSDVPADPLTSAKPSTDASFLLGAFGDDSTGIGSAPIPDILPPPQLQQPK
24643846.f MLDNFVTKPSTRS-SPPPGARKSDRVSSPLVLVDVTETAEHPLS-PMPEPSPPIIDLNLNQPSDVPADPLTSAKPSTDASFLLGAFGDDSTGIGSAPIPDILPPPQLQQPK
31202591.i NVDNDFVTKPSSARATAGESTAPQKPPRAPPSPQFMERVLGDIDIR-RGSSGTPPVVAACEREREADLNLNKNSQGRPAEEESPAWPVKIEETYDILLGLGSPVVKGAFAGSG-VRSPT
GAK.h ILISPGKELRQPGSTAQYDAGGSPEAFTSDSPSPSSADASRFHTLDWQEEKFAETGAENASSKESALMREDRSESVSDEGGSPISSEQEPRADPEPGLAAGLIVQDLDVFEVETPAVLPFEPVQEDGVLLGLHSEVGAGPAPVQACAKAPSNT-DLLSCLLGPQGPPEDILS-EDPLLLASPA
13591947.m ILISPGKELRQPGSTAQYDAGGSPEAFTSDSPSPSSADASRFHTLDWQEEKFAETGAENASSKESALMREDRSESVSDEGGSPISSEQEPRADPEPGLAAGLIVQDLDVFEVETPAVLPFEPVQEDGVLLGLHSEVGAGPAPVQACAKAPSNT-DLLSCLLGPQGPPEDILS-EDPLLLASPA
18403106.p
30685467.p
AK072774.q
AK110435.q
AK110435.w
17567783.w
2phk_PHK
113r_PKA
2erk_Erk2
1jwh_CKII
9964398.v
23509148.z IAKKEDVLINEINRNNEHDKNAITCSNEYXNLSLFYD-FWNNTKDNEFFGD-DDYDNVNKSIFIFNNLDLFDNYELCTNNNTTEKSTHHVKNNCMDINNNIFNKNYDEHVDKKEKNISYDVNVKSHPI
lias_TGFbR

1200

21356245.f -INNDPFIDFGSVDQGGVPS-MKPSGFPFVGSLPT-FVAQPAATTNPSPTHPARASADPFAANIADLATGLN-LNFNRSTLSG-KSPVNTSQPTQFSSPTHKPSPSSQPQAT-FMHTPPPTQTLFSTSSIRTPQAVPAQSRP
24643846.f -INNDPFIDFGSVDQGGVPS-MKPSGFPFVGSLPT-FVAQPAATTNPSPTHPARASADPFAANIADLATGLN-LNFNRSTLSG-KSPVNTSQPTQFSSPTHKPSPSSQPQAT-FMHTPPPTQTLFSTSSIRTPQAVPAQSRP
31202591.i -SSAVLDDIFGTLDAGAPGSTLP-TTNFGFDDAFAVGAPQSIYNSAAPAGVPSQSPAAAAAAASDFAIDIGNLAAGLGGGISAAGAAGWGG-KPGTTPPSRSTQFSPGQTPQSGASGS-TANPSR-AP-STPNHQMRSPNDPSQAQSP
GAK.h PFLSVQSTPRGGPAAADPFGPLLPSGGNNSQPCSNPDLFGEFLNS-DSVTVPPSFSAHSAPPSCSAD-FLHLGDLPGEPESKMTASSSNPDLLGGWAATETAAVASAPTPATEGLFSPGQGQAPCGSQASWTKSQNPDPFADLGLDLSQLQGSAGFPPGGFIPKTATTAKGSSSWQTSPAPQAGASWPQAKPPP
13591947.m SLLGVQSNLQCKVDETVDPDQFLPSSSDTQPCSKPDLFGEFLNS-DSVAVSSTAPFSTHAPPSCSSTA-FLHLGDLPAEPNKVIASSHPDLLGGWDITWAETALPGFASMPVPEGLTLFSSAGHPAPPGPNPSQTKSQNPDPFADLSDLSSSLQGLPAGLFGASFVGTSATTHKNSNSWQTTRPTAGTSWPPQAKPPP
18403106.p
30685467.p
AK072774.q
AK110435.q
AK110435.w
17567783.w
2phk_PHK
113r_PKA
2erk_Erk2
1jwh_CKII
9964398.v
23509148.z YSSYKNEKRCNLDIKONNSSKYIMSDKNDKFSELLDDFQKCTIK-
lias_TGFbR

1300

21356245.f DYSRLHFD-SQKAAQQPGTGGSKNSDIFADILGQQGYSFGSKMNQCPRSINEMRKEDLFKDMDPKKVRIMEWDGKNNIRALLCSMHTVLDN-AKWQRCEMSTMVTPTEVKKAYRACLAVHPDKHNGTENEELIAKLIFMEIINNAWTDFENDATQONMFNA
24643846.f DYSRLHFD-SQKAAQQPGTGGSKNSDIFADILGQQGYSFGSKMNQCPRSINEMRKEDLFKDMDPKKVRIMEWDGKNNIRALLCSMHTVLDN-AKWQRCEMSTMVTPTEVKKAYRACLAVHPDKHNGTENEELIAKLIFMEIINNAWTDFENDATQONMFNA
31202591.i DYSRLSHFEPKKNONGSAKADPAGVGGGRRSDGFDILGQQGYSFGSTKNGFRMNDKREKKEVREMDPERVKLMEWTEGKNNIRALLCTVHTWLWPG-AKWTCKEMIQLVSAADVKKYKRACLAVHPDKHGTENEEMAKMIFMELNNAWTFESDATQONLFW
GAK.h KACTOPRNYASNFWSVIG-AEERERVGRAPSFAQKPKVSENDFEDLLSNQGFSRRSDKK-GFKTIAEMRKQDIAKTDPLKLLKLLDWEICKERNIRALLSTLHTVLDGESRWTVPGMADLVAPEQVKKHYRAVLAVHPDKAAGQPYECHAKMIFMELNDAWSEFENQGSRP-LF
13591947.m RASEQLR-SHFWSVIG-AEERERVGRAPSFAQKPKVSENDFEDLLPNQGFS-KSDKK-GPKTMAEMRKQELARDTDPFKLKLDDWIECKERNIRALLSTLHTVLDGESRWTVPMSADLVTPEQVKKQYRRAVLVHHPDKATGQPYEQSAKMIFMELNDAWSEFENQGSRP-LF
18403106.p
30685467.p
AK072774.q
AK110435.q
AK110435.w
17567783.w
2phk_PHK
113r_PKA
2erk_Erk2
1jwh_CKII
9964398.v
23509148.z IAKKEDVLINEINRNNEHDKNAITCSNEYXNLSLFYD-FWNNTKDNEFFGD-DDYDNVNKSIFIFNNLDLFDNYELCTNNNTTEKSTHHVKNNCMDINNNIFNKNYDEHVDKKEKNISYDVNVKSHPI
lias_TGFbR